

```

Db 312 DIQWEDSLQIQDSWATNRQFESEBEFQTLKLLKPLSDRFLNSTALISQYWTMDSNLOHR 371
Qy 355 YEOLNSMKQLFLKAKQIVHKLPSLSKCHKQPLISLPRQRTSTYMLTRIQSPLYCNG 414
Db 372 YQQLGASLKVLLKMKHRIVRRLFNLCRCHRPRLPKERSLSFWMNRISQSLYCGEST 431
Qy 415 LIGSFSETHSCTCPNDQVCTAFIPCTVGDASACLTCAPDNRTRCTCTGTYMLSGGLC 474
Db 432 PGTFLEQSHSCTCPYDQSSCCGPIPCALGEGPACAHASDNSTRCSNPGYVLAQGLC 491
Qy 475 KPEVAESTDHYGFETDLDLEKYLKQTDRIEVAHAFISNDMLNSWDFPSWRKML 534
Db 492 RPEVAESLEHFLGLEDLDLEKYLKQTDRIEVAHAFISNDMLNSWDFPSWRKML 551
Qy 535 LTLKSNKYKSLVHMILGLSLOICLTQNSTLEPVLAVYVNPFGGSHSESFMFVNENFP 594
Db 552 LTLKSNKYKSLVHMILGLSLOICLTQNSTLEPVLAVYVNPFGGSHSESFMFVNENFP 611
Qy 595 DWERTKLDLPQCYNTLTGNKWKTFETVHYLRSRIKSNPGNESIYYPELEPIDP 654
Db 612 DWERTNVDAQAQCNWITLGNKWKTFETVHYLRSRIKSNPGNESIYYPELEPIDP 671
Qy 655 SRNLGVMKINNIQVFGYSMHFDPPEAIRDLILQDYPYTGQSDSALLQLEIRDRVNKLS 714
Db 672 SKNLGVMKINTLOVFGYSLFPDPAIRDLILQDYPYTGQSDSALLQLEIRDRVNKLS 731
Qy 715 PGQRRLDLFSCLLRHRLKSTSEVVRISQALQAFNAKLNTWYDTTKLCS 766
Db 732 PGQRRLDLFSCLLRHRLKSTSEVVRISQALQAFNAKLNTWYDTTKLCS 783

RESULT 5
Q80T96 PRELIMINARY; PRT; 788 AA.
ID Q80T96 AC Q80T96;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MKTAA1747 protein (Fragment).
CN Name=6430517E21Rik; Synonyms=MKTAA1747;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA genes:
RT cDNAs identified by screening of terminal sequences of 400 mouse KIAA-homologous
RT randomly sampled from size-fractionated libraries.";
RL DNA Ref. 10:35-48(2003).
DR EMBL; AK122549; BAC65831.1; -
DR MGD; MGI:2443333; 6430517E21Rik.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
FT NON_TER
SQ SEQUENCE 788 AA; 89748 MW; DF4189DAFD43705B CRC64;

Query Match 72.6%; Score 2963; DB 2; Length 788;
Best Local Similarity 70.7%; Ref. NO. 9.2e-205;
Matches 546; Conservative 97; Mismatches 107; Indels 22; Gaps 5;

Qy 17 LW-----IALSLCHCVLAFAA-----VSDQHATS-----PFDMLLSKGPFRHSQY 60
Db 17 LWPEAPFAVLLALGVPGHVLVSATVAAVVPEQRVSSAGQAPLDMLLTDRGFHQAQY 76

```

```

Qy 61 TDFVDSRQGFSTRYKIVREFGRWKNVNLAVERNFLGSLPLAPEFRNIRLLGRPTL 130
Db 77 ADPMERYQGFSTRYKIVREFGRWKNVNLAVERNFLGSLPLAPEFRNIRLLGRPTL 136
Qy 121 QQTITENLKKYGTHTFLLSATLGGESLTIFFVDRKLSKRAEGSDSTT-----NSSSVTL 174
Db 137 QQVTENLKKYGTHTFLLSATLGGESLTIFFVDRKLSKRAEGSDSTT-----NSSSVTL 196
Qy 175 ETLHOLAASVYDFDRSTRRLHHIOIATAIKVTETGTPLGCSNYDNLDSVSVLVQSP 234
Db 197 ETLHOLAASVYDFDRSTRRLHHIOIATAIKVTETGTPLGCSNYDNLDSVSVLVQSP 256
Qy 235 ENKIQOGLQVLLPYLQERFVQAALSVIACNSGEFTCKENDCWCCHGCPKFPCECPSM 294
Db 257 ENKVQLLGLQVLLPEHLRFRFVAALSVIITCSSEGLVCRENDCWCCKSPTFPECNCPDA 316
Qy 295 DIOAMENLRLITETWKAYNSDFEESDEFKLFMRKLPMTYFLANTSTIMHLMTWDSNFQRR 354
Db 317 DIOAMEDSLQIQDSWATNRQFESEBEFQTLKLLKPLSDRFLNSTALISQYWTMDSNLOHR 376
Qy 355 YEOLNSMKQLFLKAKQIVHKLPSLSKCHKQPLISLPRQRTSTYMLTRIQSPLYCNG 414
Db 377 YQQLGASLKVLLKMKHRIVRRLFNLCRCHRPRLPKERSLSFWMNRISQSLYCGEST 436
Qy 415 LIGSFSETHSCTCPNDQVCTAFIPCTVGDASACLTCAPDNRTRCTCTGTYMLSGGLC 474
Db 437 PGTFLEQSHSCTCPYDQSSCCGPIPCALGEGPACAHASDNSTRCSNPGYVLAQGLC 496
Qy 475 KPEVAESTDHYGFETDLDLEKYLKQTDRIEVAHAFISNDMLNSWDFPSWRKML 534
Db 497 RPEVAESLEHFLGLEDLDLEKYLKQTDRIEVAHAFISNDMLNSWDFPSWRKML 556
Qy 535 LTLKSNKYKSLVHMILGLSLOICLTQNSTLEPVLAVYVNPFGGSHSESFMFVNENFP 594
Db 557 LTLKSNKYKSLVHMILGLSLOICLTQNSTLEPVLAVYVNPFGGSHSESFMFVNENFP 616
Qy 595 DWERTKLDLPQCYNTLTGNKWKTFETVHYLRSRIKSNPGNESIYYPELEPIDP 654
Db 617 DWERTNVDAQAQCNWITLGNKWKTFETVHYLRSRIKSNPGNESIYYPELEPIDP 676
Qy 655 SRNLGVMKINNIQVFGYSMHFDPPEAIRDLILQDYPYTGQSDSALLQLEIRDRVNKLS 714
Db 677 SKNLGVMKINTLOVFGYSLFPDPAIRDLILQDYPYTGQSDSALLQLEIRDRVNKLS 736
Qy 715 PGQRRLDLFSCLLRHRLKSTSEVVRISQALQAFNAKLNTWYDTTKLCS 766
Db 737 PGQRRLDLFSCLLRHRLKSTSEVVRISQALQAFNAKLNTWYDTTKLCS 788

RESULT 6
Q95560 PRELIMINARY; PRT; 781 AA.
ID Q95560 AC Q95560;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes S.; (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-1999); CAA2893.1; -
DR EMBL; AL035289; CAA2893.1; -
DR InterPro; IPR006210; IEGF.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
DR Hypothetical protein.
FT NON_TER

```

SO SEQUENCE 781 AA; 88216 MW; DFE3EB83A088B599 CRC64;  
 Query Match 72.6%; Score 2962; DB 2; Length 781;  
 Best Local Similarity 70.6%; Pred. No. 1.1e-204;  
 Matches 543; Conservative 99; Mismatches 109; Indels 18; Gaps 4;

QY 16 ALMEW---IALSLHCWLVAA-----VSDQAT-----SPFDWLLSDKGFPHRSOBYTDF 63  
 DB 13 AVAPMTALLALGLPGWLVASATAAAVPEQHASVAGQHPDLWLLTDGPFHRAQYADP 74  
 QY 64 VDRSQCFSTRYKIYREFGKWKNNLAVERRNPLGSPPLAPEPFNRLGLRRPTLOOI 123  
 DB 73 MERYRQGFTRYRIYREFARWKNNIALERKOFFSPLPLAPEPFNRLGLRRRNLOOV 134  
 QY 124 TENLIKKGTHFLLSATLGGESLTFVDRKLSKRAEGSDSTT-----NSSSVTLETL 177  
 DB 135 TENLIKKGTHFLLSATLGGESLTFVDRKLSKRAEGSDSTT-----NSSSVTLETL 194  
 QY 178 HOLAAASYFIDRSDTLRLRHIIQIATAIKVTETCTGPGCCSNYDNLDSVSVLVOSPENK 237  
 DB 195 HOLAAASYFIDRSDTLRLRHIIQIATAIKVTETCTGPGCCSNYDNLDSVSVLVOSPENK 254  
 QY 238 IQLOGLOVLLPDYLOERFVOAALSYIACNSEGEFICKENDCWCCHGCKPPECNCPSMDIQ 297  
 DB 255 VOLGLQVLLPEYLRERFVAALSYIACNSEGEFICKENDCWCCHGCKPPECNCPSMDIQ 314  
 QY 298 AMEENLRITETWKAYNSDFEESDEPKLPMQCLPMNYFLNTSTIMHLMTMDSNFORRYEQ 357  
 DB 315 AMEDSLQIODSWATHNRQFESEEFQALLKRLPDDRFLNSTAISQFAMDTSLQHRVQO 374  
 QY 358 LENSXKQFLKAAKIVHKLPSLRCHKOPILSLPRORTSTYMLTRIQSFYCHENGLLG 417

RESULT 7  
 Q8N360 PRELIMINARY; PRT; 783 AA.  
 AC Q8N360;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 25-OCT-2004 (TRENBLrel. 22, Last annotation update)  
 DE BMP/retinoic acid-inducible neutral-specific protein 2 (DBCCRI-like2).  
 GN Name=KIAA1747; Synonyms=DBCCRI2;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;

SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schuetz T.E., Brownstein M.J., Usdin T.B., Tohizuki S., Carninci P., Prange C., Raha S.S., Loughran N.A., Peters K.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myer R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Small U., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 (2)

SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RC Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 (3)

SEQUENCE FROM N.A.  
 RP Inazawa J., Imoto I.;  
 RT "Homo sapiens DBCCRI2 mRNA for DBCCRI-like2";  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC028036; AAH28036.1; -;  
 DR EMBL; AB161694; BAD34946.1; -;  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001862; MAC\_perforin.  
 DR Pfam; PF01823; MACPF; 1.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00457; MACPF; 1.  
 SQ SEQUENCE 783 AA; 89004 MW; B8362095ADC97FCD CRC64;

Query Match 72.6%; Score 2962; DB 2; Length 783;  
 Best Local Similarity 70.6%; Pred. No. 1.1e-204;  
 Matches 543; Conservative 99; Mismatches 109; Indels 18; Gaps 4;

QY 16 ALMEW---IALSLHCWLVAA-----VSDQAT-----SPFDWLLSDKGFPHRSOBYTDF 63  
 DB 15 AVAPMTALLALGLPGWLVASATAAAVPEQHASVAGQHPDLWLLTDGPFHRAQYADP 74  
 QY 64 VDRSQCFSTRYKIYREFGKWKNNLAVERRNPLGSPPLAPEPFNRLGLRRPTLOOI 123  
 DB 75 MERYRQGFTRYRIYREFARWKNNIALERKOFFSPLPLAPEPFNRLGLRRRNLOOV 134  
 QY 124 TENLIKKGTHFLLSATLGGESLTFVDRKLSKRAEGSDSTT-----NSSSVTLETL 177  
 DB 135 TENLIKKGTHFLLSATLGGESLTFVDRKLSKRAEGSDSTT-----NSSSVTLETL 194  
 QY 178 HOLAAASYFIDRSDTLRLRHIIQIATAIKVTETCTGPGCCSNYDNLDSVSVLVOSPENK 237  
 DB 195 HOLAAASYFIDRSDTLRLRHIIQIATAIKVTETCTGPGCCSNYDNLDSVSVLVOSPENK 254  
 QY 238 IQLOGLOVLLPDYLOERFVOAALSYIACNSEGEFICKENDCWCCHGCKPPECNCPSMDIQ 297  
 DB 255 VOLGLQVLLPEYLRERFVAALSYIACNSEGEFICKENDCWCCHGCKPPECNCPSMDIQ 314  
 QY 298 AMEENLRITETWKAYNSDFEESDEPKLPMQCLPMNYFLNTSTIMHLMTMDSNFORRYEQ 357  
 DB 315 AMEDSLQIODSWATHNRQFESEEFQALLKRLPDDRFLNSTAISQFAMDTSLQHRVQO 374  
 QY 358 LENSXKQFLKAAKIVHKLPSLRCHKOPILSLPRORTSTYMLTRIQSFYCHENGLLG 417